AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Claims 1-15 (Cancelled).

16. (Previously Presented) An isolated nucleic acid comprising a nucleotide sequence encoding the effector domain of the binding molecule as claimed in claim 32, wherein said nucleic acid is DNA.

17. (Previously Presented) An isolated nucleic acid comprising a nucleotide sequence encoding the binding molecule as claimed in claim 32, wherein said nucleic acid is DNA.

18. (Previously Presented) The nucleic acid as claimed in claim 16 which is a replicable vector.

19. (Previously Presented) The nucleic acid as claimed in claim 18 wherein the nucleotide sequence is operably linked to a promoter.

20. (Previously Presented) A host cell comprising or transformed with the vector of claim 19.

21. (Previously Presented) A process for producing a binding molecule which is a recombinant polypeptide comprising:

(i) a binding domain capable of binding a target molecule, which binding domain is the binding site of an antibody, and

(ii) an effector domain having an amino acid sequence homologous to a constant domain of a human immunoglobulin heavy chain;

wherein the binding molecule is capable of binding the target molecule without triggering significant complement dependent lysis, or cell mediated destruction of the target, and the effector domain is capable of specifically binding FcγRIIb and optionally FcRn,

and wherein the effector domain comprises a chimeric C_H2 domain which is derived from two or more human immunoglobulin heavy chain C_H2 domains, which human immunoglobulins are selected from IgG1, IgG2 and IgG4,

and wherein the effector domain has a reduced affinity for FcγRI, FcγRIIa and FcγRIII and a reduced ability to mediate complement lysis by comparison with said constant domain of a human immunoglobulin heavy chain;

the process comprising the step of modifying a nucleotide sequence encoding a first human immunoglobulin heavy chain C_H2 domain such that 2, 3 or 4 amino acids in at least 1 region of the C_H2 domain correspond to the amino acids from a second human immunoglobulin heavy chain C_H2 domain,

wherein said modification introduces the following blocks of amino acids at the stated positions: 233P, 234V, 235A, 236G, 327G, 330S and 331S numbered with respect to the EU numbering system of Kabat

and wherein in said chimeric C_H2 domain is at least 98% identical to a C_H2 sequence (residues 231-340) from human IgG1 or IgG4 having said modified amino acids.

22. (Previously Presented) The process as claimed in claim 21 wherein 2 amino acids in 1 region of the C_H2 domain are modified to the corresponding amino acids from the second human immunoglobulin heavy chain C_H2 domain.

23. (Currently Amended) A method of binding a target molecule, which target molecule is capable of being bound by said binding molecule of claim 32, said method comprising contacting said target molecule with ~~a~~ the binding molecule of claim 32 under conditions that ~~allowing~~ allow binding.

24. (Currently Amended) The method of claim 23 wherein the effector domain of said binding molecule of claim 32 binds ~~target molecule is~~ FcγRIIb, which binding causes inhibition of one or more of: B cell activation; mast cell degranulation; and phagocytosis.

25. (Currently Amended) The method of claim ~~24~~ 23 to prevent, inhibit, or otherwise interfere with the binding of a second binding molecule to the target molecule.

26. (Previously Presented) The method of claim 25 wherein the second binding molecule is an antibody.

27. (Currently Amended) The method of claim ~~25~~ 23 wherein the target molecule is selected from: the RhD antigen of red blood cells; an HPA alloantigen of platelets; a neutrophil antigen; a T-cell receptor; integrin; GBM collagen; Der P1; HPA-1a; VAP-1; laminin; lutheran; platelet glycoprotein VI; platelet glycoprotein Ia/IIa.

28. (Currently Amended) ~~A~~ The method of claim ~~24~~ 23 for the treatment of a patient:

i) for a disorder selected from the group consisting of: ~~Graft-vs-host disease; host-vs-graft disease; organ transplant rejection; bone marrow transplant rejection; autoimmunity such as vasculitis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia and arthritis; alloimmunity such as foetal/neonatal alloimmune thrombocytopenia; asthma and allergy; chronic or acute inflammatory diseases such as Chrohn's; HDN; Goodpastures, sickle cell anaemia, coronary artery occlusion~~

ii) Graft-vs-host disease, host-vs-graft disease, organ transplant rejection, bone-marrow transplant rejection, autoimmune vasculitis, arthritis and asthma, wherein the target molecule is a T-cell receptor;

ii) for a disorder selected from the group consisting of autoimmune haemolytic anaemia and autoimmune thrombocytopenia, wherein the target molecule is selected from the group consisting of red blood cell Rhesus antigens D,C,c,E and e, the Kell (K1) antigen and platelet glycoprotein GPIIb/IIIa and GPIb/IX/V;

iii) for foetal/neonatal alloimmune thrombocytopenia, wherein the target molecule is human platelet antigen (HPA)-1a or platelet glycoprotein IIIa;

iv) for dust mite allergy, wherein the target molecule is Der P1 protein of the house dust mite Dermatophagoides pteronyssinus;

v) for Chrohn's, wherein the target molecule is VAP-1;

vi) for HDN, wherein the target molecule is selected from the group consisting of red blood cell Rhesus antigens D,C,c,E and e, and the Kell (K1) antigen;

vii) for Goodpastures, wherein the target molecule is non-collagenous (NC1) domain of α3(IV) collagen;

viii) for sickle cell anaemia, wherein the target molecule is selected from the group consisting of: thrombospondin, laminin and lutheran; or

ix) for coronary artery occlusion, wherein the target molecule is selected from the group consisting of integrin $\alpha_2\beta_1$ (platelet glycoprotein Ia/IIa) and non-integrin platelet glycoprotein VI.

29. (Previously Presented) The method of claim 23 wherein the binding molecule is administered to a patient, or optionally in cases where the patient is an unborn infant, to the mother of the patient.

Claim 30 (Canceled).

31. (Withdrawn) An oligonucleotide selected from:

MO22BACK: 5' TCT CCA ACA AAG GCC TCC CGT CCT CCA TCG AGA AAA 3' (SEQ ID NO:16)

MO22: 5' TTT TCT CGA TGG AGG ACG GGA GGC CTT TGT TGG AGA 3' (SEQ ID NO:17)

MO7BACK: 5' TCC TCA GCA CCT CCA GTC GCG GGG GGA CCG TCA GTC 3' (SEQ ID NO:18)

MO21: 5' GAC TGA CGG TCC CGC GAC TGG AGG TGC TGA GGA 3' (SEQ ID NO:19)

32. (Previously Presented) A binding molecule which is a recombinant polypeptide comprising:

(i) a binding domain capable of binding a target molecule, which binding domain is the binding site of an antibody, and

(ii) an effector domain having an amino acid sequence homologous to a constant domain of a human immunoglobulin heavy chain;

wherein the binding molecule is capable of binding the target molecule without triggering significant complement dependent lysis, or cell mediated destruction of the target, and the effector domain is capable of specifically binding FcγRIIb and optionally FcRn,

and wherein the effector domain comprises a chimeric C_H2 domain which is derived from two or more human immunoglobulin heavy chain C_H2 domains, which human immunoglobulins are selected from IgG1, IgG2 and IgG4,

and wherein the effector domain has a reduced affinity for FcγRI, FcγRIIa and FcγRIII and a reduced ability to mediate complement lysis by comparison with said constant domain of a human immunoglobulin heavy chain

and wherein the chimeric C_H2 domain is a human immunoglobulin heavy chain C_H2 domain which has the following blocks of amino acids at the stated positions: 233P, 234V, 235A, 236G, 327G, 330S and 331S numbered with respect to the EU numbering system of

Kabat, and is at least 98% identical to a C_H2 sequence (residues 231-340) from human IgG1 or IgG4 having said modified amino acids.

33. (Currently Amended) The binding molecule as claimed in claim 32 wherein the chimeric C_H2 domain ~~comprises~~ consists of G1Δac (SEQ ID NO:3) or G4Δc (SEQ ID NO:12) as shown in Figure 17.

Claims 34-36 (Cancelled).

37. (Previously Presented) The binding molecule as claimed in claim 32 wherein the binding domain derives from a different source to the effector domain.

38. (Previously Presented) The binding molecule as claimed in claim 32 wherein the binding domain is capable of binding any of: the RhD antigen of red blood cells; an HPA alloantigen of platelets; a neutrophil antigen; a T-cell receptor; integrin; GBM collagen; Der P1; HPA-1a; VAP-1; laminin; lutheran; platelet glycoprotein VI; platelet glyprotein Ia/IIa.

39. (Previously Presented) The binding molecule as claimed in claim 38 wherein the binding domain is selected from anti-CD52 antigen found on human lymphocytes; anti-RhD; anti-HPA-1a; anti-VAP-1; murine anti-α3 (IV) NC1; anti-CD3; anti-Der p I; anti-laminin; anti-lutheran.

40. (Currently Amended) A ~~pharmaceutical~~ preparation comprising a binding molecule as claimed in claim 32 plus a pharmaceutically acceptable carrier.

41. (Previously Presented) A binding molecule which is a recombinant polypeptide comprising:

(i) a binding domain capable of binding a target molecule, which binding domain is the binding site of an antibody, and

(ii) an effector domain having an amino acid sequence homologous to a constant domain of a human immunoglobulin heavy chain;

wherein the binding molecule is capable of binding the target molecule without triggering significant complement dependent lysis, or cell mediated destruction of the target, and the effector domain is capable of specifically binding FcγRIIb and optionally FcRn,

and wherein the effector domain comprises a chimeric C_H2 domain which is derived from two or more human immunoglobulin heavy chain C_H2 domains, which human immunoglobulins are selected from IgG1, IgG2 and IgG4,

and wherein the effector domain has a reduced affinity for FcγRI, FcγRIIa and FcγRIII and a reduced ability to mediate complement lysis by comparison with said constant domain of a human immunoglobulin heavy chain

and wherein the chimeric C_H2 domain is a human immunoglobulin heavy chain C_H2 domain which has the following blocks of amino acids at the stated positions: 233P, 234V, 235A and no residue at 236, 327G, 330S and 331S, numbered with respect to the EU system of Kabat, and is at least 98% identical to a C_H2 sequence (residues 231-340) from human IgG1 or IgG2 having said modified amino acids.

42. (Currently Amended) The binding molecule as claimed in claim 41 wherein the chimeric C_H2 domain ~~comprises~~ consists of G1Δab (SEQ ID NO:1) or G2Δa (SEQ ID NO:2) as shown in Figure 17.

Claims 43-45 (Cancelled).

46. (Previously Presented) The binding molecule as claimed in claim 41 wherein the binding domain derives from a different source to the effector domain.

47. (Previously Presented) The binding molecule as claimed in claim 41 wherein the binding domain is capable of binding any of: the RhD antigen of red blood cells; an HPA alloantigen of platelets; a neutrophil antigen; a T-cell receptor; integrin; GBM collagen; Der P1; HPA-1a; VAP-1; laminin; lutheran; platelet glycoprotein VI; platelet glyprotein Ia/IIa.

48. (Previously Presented) The binding molecule as claimed in claim 47 wherein the binding domain is selected from that of anti-CD52 antigen found on human lymphocytes; anti-RhD; anti-HPA-1a; anti-VAP-1; murine anti-α3 (IV) NC1; anti-CD3; anti-Der p I; anti-laminin; anti-lutheran.

49. (Currently Amended) A ~~pharmaceutical~~ preparation comprising a binding molecule as claimed in claim 41 plus a pharmaceutically acceptable carrier.

50. (Previously Presented) An isolated nucleic acid comprising a nucleotide sequence encoding the effector domain of the binding molecule as claimed in claim 41, wherein said nucleic acid is DNA.

51. (Previously Presented) An isolated nucleic acid comprising a nucleotide sequence encoding the binding molecule as claimed in claim 41, wherein said nucleic acid is DNA.

52. (Previously Presented) The nucleic acid as claimed in claim 50 which is a replicable vector.

53. (Previously Presented) The nucleic acid as claimed in claim 52 wherein the nucleotide sequence is operably linked to a promoter.

54. (Previously Presented) A host cell comprising or transformed with the vector of claim 53.

55. (Previously Presented) A process for producing a binding molecule which is a recombinant polypeptide comprising:

(i) a binding domain capable of binding a target molecule, which binding domain is the binding site of an antibody, and

(ii) an effector domain having an amino acid sequence homologous to a constant domain of a human immunoglobulin heavy chain;

wherein the binding molecule is capable of binding the target molecule without triggering significant complement dependent lysis, or cell mediated destruction of the target, and the effector domain is capable of specifically binding FcγRIIb and optionally FcRn,

and wherein the effector domain comprises a chimeric C_H2 domain which is derived from two or more human immunoglobulin heavy chain C_H2 domains, which human immunoglobulins are selected from IgG1, IgG2 and IgG4,

and wherein the effector domain has a reduced affinity for FcγRI, FcγRIIa and FcγRIII and a reduced ability to mediate complement lysis by comparison with said constant domain of a human immunoglobulin heavy chain;

the process comprising the step of modifying a nucleotide sequence encoding a first human immunoglobulin heavy chain C_H2 domain such that 2, 3 or 4 amino acids in at least 1 region of the C_H2 domain correspond to the amino acids from a second human immunoglobulin heavy chain C_H2 domain,

wherein said modification introduces the following blocks of amino acids at the stated positions: 233P, 234V, 235A, 236G, 327G, 330S and 331S numbered with respect to the EU numbering system of Kabat

and wherein in said chimeric C_H2 domain is at least 98% identical to a C_H2 sequence (residues 231-340) from human IgG1 or IgG4 having said modified amino acids.

56. (Previously Presented) The process as claimed in claim 55 wherein 2 amino acids in 1 region of the C_H2 domain are modified to the corresponding amino acids from the second human immunoglobulin heavy chain C_H2 domain.

57. (Currently Amended) A method of binding a target molecule, which target molecule is capable of being bound by said binding molecule of claim 41, said method comprising contacting said target molecule with ~~a~~ said binding molecule of claim 41 under conditions that ~~allowing~~ allow binding.

58. (Currently Amended) The method of claim 57 wherein the effector domain of said binding molecule of claim 41 specifically binds ~~target molecule is~~ FcγRIIb, which binding causes inhibition of one or more of: B cell activation; mast cell degranulation; and phagocytosis.

59. (Currently Amended) The method of claim ~~58~~ 57 to prevent, inhibit, or otherwise interfere with the binding of a second binding molecule to the target molecule.

60. (Previously Presented) The method of claim 59 wherein the second binding molecule is an antibody.

61. (Currently Amended) The method of claim ~~59~~ 57 wherein the target molecule is selected from: the RhD antigen of red blood cells; an HPA alloantigen of platelets; a neutrophil antigen; a T-cell receptor; integrin; GBM collagen; Der P1; HPA-1a; VAP-1; laminin; lutheran; platelet glycoprotein VI; platelet glycoprotein Ia/IIa.

62. (Currently Amended) The method of claim ~~58~~ 57 for the treatment of a patient:

i) for a disorder selected from the group consisting of: ~~Graft vs host disease; host vs graft disease; organ transplant rejection; bone marrow transplant rejection; autoimmunity~~

~~such as vasculitis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia and arthritis; alloimmunity such as foetal/neonatal alloimmune thrombocytopenia; asthma and allergy; chronic or acute inflammatory diseases such as Chrohn's; HDN; Goodpastures, sickle cell anaemia, coronary artery ocolusion~~ .

ii) Graft-vs-host disease, host-vs-graft disease, organ transplant rejection, bone-marrow transplant rejection, autoimmune vasculitis, arthritis and asthma, wherein the target molecule is a T-cell receptor;

ii) for a disorder selected from the group consisting of autoimmune haemolytic anaemia and autoimmune thrombocytopenia, wherein the target molecule is selected from the group consisting of red blood cell Rhesus antigens D,C,c,E and e, the Kell (K1) antigen and platelet glycoprotein GPIIb/IIIa and GPIb/IX/V;

iii) for foetal/neonatal alloimmune thrombocytopenia, wherein the target molecule is human platelet antigen (HPA)-1a or platelet glycoprotein IIIa;

iv) for dust mite allergy, wherein the target molecule is Der P1 protein of the house dust mite Dermatophagoides pteronyssinus;

v) for Chrohn's, wherein the target molecule is VAP-1;

vi) for HDN, wherein the target molecule is selected from the group consisting of red blood cell Rhesus antigens D,C,c,E and e, and the Kell (K1) antigen;

vii) for Goodpastures, wherein the target molecule is non-collagenous (NC1) domain of α3(IV) collagen;

viii) for sickle cell anaemia, wherein the target molecule is selected from the group consisting of: thrombospondin, laminin and lutheran; or

ix) for coronary artery occlusion, wherein the target molecule is selected from the group consisting of integrin $\alpha_2\beta_1$ (platelet glycoprotein Ia/IIa) and non-integrin platelet glycoprotein VI.

63. (Previously Presented) The method of claim 57 wherein the binding molecule is administered to a patient, or optionally in cases where the patient is an unborn infant, to the mother of the patient.

64. (Previously Presented) The binding molecule as claimed in claim 39 wherein the anti-CD52 binding domain is CAMPATH-1; the anti-RhD is FOG1; the anti-Der p I is 2C7; the anti-CD3 is YTH12.5.

65. (Previously Presented) The binding molecule as claimed in claim 48 wherein the anti-CD52 binding domain is CAMPATH-1; the anti-RhD is FOG1; the anti-Der p I is 2C7; the anti-CD3 is YTH12.5.

66. (Previously Presented) A process for producing a binding molecule which is a recombinant polypeptide comprising:

(i) a binding domain capable of binding a target molecule, which binding domain is the binding site of an antibody, and

(ii) an effector domain having an amino acid sequence homologous to a constant domain of a human immunoglobulin heavy chain;

wherein the binding molecule is capable of binding the target molecule without triggering significant complement dependent lysis, or cell mediated destruction of the target, and the effector domain is capable of specifically binding FcγRIIb and optionally FcRn,

and wherein the effector domain comprises a chimeric C_H2 domain which is derived from two or more human immunoglobulin heavy chain C_H2 domains, which human immunoglobulins are selected from IgG1, IgG2 and IgG4,

and wherein the effector domain has a reduced affinity for FcγRI, FcγRIIa and FcγRIII and a reduced ability to mediate complement lysis by comparison with said constant domain of a human immunoglobulin heavy chain;

the process comprising the step of modifying a nucleotide sequence encoding a first human immunoglobulin heavy chain C_H2 domain such that 2, 3 or 4 amino acids in at least 1 region of the C_H2 domain correspond to the amino acids from a second human immunoglobulin heavy chain C_H2 domain,

wherein said modification introduces the following blocks of amino acids at the stated positions: 233P, 234V, 235A and no residue at 236, 327G, 330S and 331S numbered with respect to the EU numbering system of Kabat

and wherein said chimeric C_H2 domain is at least 98% identical to a C_H2 sequence (residues 231-340) from human IgG1 or IgG2 having said modified amino acids,

67. (Previously Presented) The process as claimed in claim 66 wherein 2 amino acids in 1 region of the C_H2 domain are modified to the corresponding amino acids from the second human immunoglobulin heavy chain C_H2 domain.